

[illegible]

(1)

(j)

~~(i)~~

(iii)

(iv)

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
CECCHI, STEWART & OLSTEIN

(C) CITY: ROSELAND

(D) STATE: NEW JERSEY

(E) COUNTRY: USA

(F) ZIP: 07068

(v)

(A) MEDIUM /TYPE: 3.5 INCH DISKETTE

(B) ~~COMPUTER~~: IBM PS/2

(C) OPERATING SYSTEM: MS-DOS

(D) ~~SOFTWARE~~: WORD PERFECT 5.1

## (vi)

(A) APPLICATION NUMBER:

(B) ~~F~~ILING DATE: concurrently

(C) / CLASSIFICATION:

(vii)

(A) NAME: FERRARO, GREGORY D.

(B) REGISTRATION NUMBER: 36,134

(C) REFERENCE/DOCKET NUMBER: 325800-

## (viii)

(A) TELEPHONE: 201-994-1700

(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 666 BASE PAIRS  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGAAGGT GTAGAATAAG TGGGAGGCC CCGGCGCCCC CCGGTGTCCC CGCCCAGGCC 60  
CCTGTCTCCC AGCCTGATGC CCCTGGCCAC CAGAGGAAAG TGGTGTTCATG GATAGATGTG 120  
TATACTCGCG CTACCTGCCA GCCCCGGGAG GTGGTGGTGC CCTTGACTGT GGAGCTCATG 180  
GGCACCCTGG CCAAACAGCT GGTGCCCAGC TGCCTGACTG TGCAGCGCTG TGGTGGCTGC 240  
TGCCCTGACG ATGGCCTGGA GTGTGTGCCC ACTGGGCAGC ACCAAGTCCG GATGCAGATC 300  
CTCATGATCC GGTACCCGAG CAGTCAGCTG GGGGAGATGT CCCTGGAAGA ACACAGCCAG 360  
TGTGAATGCA GACCTAAAA AAAGGACAGT GCTGTGAAGC CAGACAGGGC TGCTACTCCC 420  
CACCACCGTC CCCAGCCCCG TTCTGTTCCTG GGCTGGGACT CTGCCCCCGG AGCACCCCTCC 480  
CCAGCTGACA TCACCCATC CCACTCCAGC CCCAGGCCCC TCTGCCCACG CTGCACCCAG 540  
CACCACCACT GCCCTGACCC CCGGACCTGC CGCTGCCGCT GTCGACGCCG CAGCTTCCTC 600  
CGTTGTCAAG GGCGGGGCTT AGAGCTCAAC CCAGACACCT GCAGGTGCCG GAAGCTGCGA 660  
AGGTGA 666

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 221 AMINO ACIDS  
(B) TYPE: AMINO ACID  
(C) STRANDEDNESS:  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly  
5 10 15  
Val Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His  
20 25 30  
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr  
35 40 45  
Cys Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met  
50 55 60  
Gly Thr Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln  
65 70 75  
Arg Cys Gly Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro  
80 85 90  
Thr Gly Gln His Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr  
95 100 105  
Pro Ser Ser Gln Leu Gly Glu Met Ser Leu Glu Glu His Ser Gln  
110 115 120  
Cys Glu Cys Arg Pro Lys Lys Lys Asp Ser Ala Val Lys Pro Asp  
125 130 135  
Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro  
140 145 150  
Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr  
155 160 165  
Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro Arg Cys Thr Gln  
170 175 180  
His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys Arg Cys Arg  
185 190 195  
Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu Asn  
200 205 210  
Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg  
215 220